

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bryan, Bruce

(ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4250 Executive Square, 7th Floor
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/757,046
(B) FILING DATE: 11-25-96
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/597,274
(B) FILING DATE: 02-06-96

(ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24727-105C

(x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-450-8400
(B) TELEFAX: 619-450-8499
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...942

(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG	48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg	
1 5 10 15	
ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT	96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val	
20 25 30	
CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT	144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn	
35 40 45	
GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA	192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg	
50 55 60	
CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT	240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp	
65 70 75 80	
CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG	288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg	
85 90 95	
TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT	336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile	
100 105 110	
TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG	384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu	
115 120 125	
GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT	432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val	
130 135 140	
CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT	480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro	
145 150 155 160	
GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA	528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys	
165 170 175	
ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA	576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys	
180 185 190	
ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA	624
Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro	
195 200 205	
TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT	672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg	
210 215 220	
GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT	720

Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val		
225 230 235 240		
AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG		768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met		
245 250 255		
TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC		816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly		
260 265 270		
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT		864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His		
275 280 285		
TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG		912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser		
290 295 300		
TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA TTACTTTGGT TTTTTATTTA		965
Phe Val Glu Arg Val Leu Lys Asn Glu Gln		
305 310		
CATTTTTCCC GGGTTTAATA ATATAAATGT CATTTCACAC AATTTTATTT TAACTGAATA		1025
TTTCACAGGG AACATTCTATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC		1085
ATTTTGGAAAT ATTACCTCTT TCAATGAAAC TTTATAAACCA GTGGTTCAAT TAATTAATAT		1145
ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTA TTATAAAAAAA A		1196

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorfii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC		48
Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val		
1 5 10 15		
AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA		96
Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr		
20 25 30		
CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT		144
Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp		
35 40 45		
ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT		192
Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys		
50 55 60		

GAA	AAT	AAA	CCA	GGG	AAG	ACA	TGC	TGT	AGA	ATG	TGC	CAG	TAT	GTA	ATT	240
Glu	Asn	Lys	Pro	Gly	Lys	Thr	Cys	Cys	Arg	Met	Cys	Gln	Tyr	Val	Ile	
65				70						75					80	
GAA	TCC	AGA	GTA	GAA	GCT	GCT	GGG	TAT	TTT	AGA	ACG	TTT	TAC	GCC	AAA	288
Glu	Ser	Arg	Val	Glu	Ala	Ala	Gly	Tyr	Phe	Arg	Thr	Phe	Tyr	Ala	Lys	
85				90						95						
AGA	TTT	AAT	TTT	CAG	GAA	CCT	GGT	AAA	TAT	GTG	CTG	GCT	CGA	GGA	ACC	336
Arg	Phe	Asn	Phe	Gln	Glu	Pro	Gly	Lys	Tyr	Val	Leu	Ala	Arg	Gly	Thr	
100									105					110		
AAG	GGT	GGC	GAC	TGG	TCT	GTA	ACC	CTC	ACC	ATG	GAG	AAT	CTA	GAT	GGA	384
Lys	Gly	Gly	Asp	Trp	Ser	Val	Thr	Leu	Thr	Met	Glu	Asn	Leu	Asp	Gly	
115							120				125					
CAG	AAG	GGA	GCT	GTA	CTG	ACT	AAG	ACA	ACA	CTG	GAG	GTA	GTA	GGA	GAC	432
Gln	Lys	Gly	Ala	Val	Leu	Thr	Lys	Thr	Thr	Leu	Glu	Val	Val	Gly	Asp	
130							135				140					
GTA	ATA	GAC	ATT	ACT	CAA	GCT	ACT	GCA	GAT	CCT	ATC	ACA	GTT	AAC	GGA	480
Val	Ile	Asp	Ile	Thr	Gln	Ala	Thr	Ala	Asp	Pro	Ile	Thr	Val	Asn	Gly	
145							150			155				160		
GGA	GCT	GAC	CCA	GTT	ATC	GCT	AAC	CCG	TTC	ACA	ATT	GGT	GAG	GTG	ACC	528
Gly	Ala	Asp	Pro	Val	Ile	Ala	Asn	Pro	Phe	Thr	Ile	Gly	Glu	Val	Thr	
165									170					175		
ATT	GCT	GTT	GTC	GAA	ATA	CCC	GGC	TTC	AAT	ATT	ACA	GTC	ATC	GAA	TTC	576
Ile	Ala	Val	Val	Glu	Ile	Pro	Gly	Phe	Asn	Ile	Thr	Val	Ile	Glu	Phe	
180									185					190		
TTT	AAA	CTA	ATC	GTG	ATA	GAT	ATT	CTG	GGA	GGA	AGA	TCT	GTG	AGA	ATT	624
Phe	Lys	Leu	Ile	Val	Ile	Asp	Ile	Leu	Gly	Gly	Arg	Ser	Val	Arg	Ile	
195							200				205					
GCT	CCA	GAC	ACA	GCA	AAC	AAA	GGA	CTG	ATA	TCT	GGT	ATC	TGT	GGT	AAT	672
Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
210							215				220					
CTG	GAG	ATG	AAT	GAC	GCT	GAT	GAC	TTT	ACT	ACA	GAC	GCA	GAT	CAG	CTG	720
Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
225							230			235				240		
GCG	ATC	CAA	CCC	AAC	ATA	AAC	AAA	GAG	TTC	GAC	GGC	TGC	CCA	TTC	TAC	768
Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
245									250					255		
GGG	AAT	CCT	TCT	GAT	ATC	GAA	TAC	TGC	AAA	GGT	CTC	ATG	GAG	CCA	TAC	816
Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
260								265					270			
AGA	GCT	GTA	TGT	CGT	AAC	AAT	ATC	AAC	TTC	TAC	TAT	TAC	ACT	CTG	TCC	864
Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Tyr	Thr	Leu	Ser
275							280				285					
TGC	GCC	TTC	GCT	TAC	TGT	ATG	GGA	GGA	GAA	GAA	AGA	GCT	AAA	CAC	GTC	912
Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Glu	Arg	Ala	Lys	His	Val	
290							295				300					
CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCA	CCG	GAA	ACG	AGA	GGA	ACG	960
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
305							310			315				320		
TGT	GTT	TTA	TCA	GGA	CAT	ACT	TTC	TAT	GAC	ACA	TTC	GAC	AAA	GCC	AGA	1008

Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg			
325	330	335	
TAT CAA TTC CAG GGC CCA TGC AAA GAG CTT CTG ATG GCC GCA GAC TGT			1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Leu Leu Met Ala Ala Asp Cys			
340	345	350	
TAC TGG AAC ACA TGG GAT GTA AAG GTT TCA CAT AGA GAT GTT GAG TCA			1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser			
355	360	365	
TAC ACT GAG GTA GAG AAA GTA ACA ATC AGG AAA CAG TCA ACT GTA GTA			1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val			
370	375	380	
GAT TTG ATT GTG GAT GGC AAG CAG GTC AAG GTT GGA GGA GTG GAT GTA			1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val			
385	390	395	400
TCT ATC CCG TAC AGT TCT GAG AAC ACA TCC ATA TAC TGG CAG GAT GGA			1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly			
405	410	415	
GAC ATC CTG ACG ACG GCC ATC CTA CCT GAA GCT CTT GTC GTT AAG TTC			1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe			
420	425	430	
AAC TTT AAG CAG CTC CTT GTA GTT CAT ATC AGA GAT CCA TTC GAT GGA			1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly			
435	440	445	
AAG ACA TGC GGC ATA TGT GGT AAC TAT AAT CAA GAT TCA ACT GAT GAT			1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp			
450	455	460	
TTC TTT GAC GCA GAA GGA GCA TGC GCT CTG ACC CCC AAT CCC CCA GGA			1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly			
465	470	475	480
TGT ACA GAG GAG CAG AAA CCA GAA GCT GAG CGA CTC TGC AAT AGT CTA			1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu			
485	490	495	
TTT GAT AGT TCT ATC GAC GAG AAA TGT AAT GTC TGC TAC AAG CCT GAC			1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp			
500	505	510	
CGT ATT GCA CGA TGT ATG TAC GAG TAT TGC CTG AGG GGA CAG CAA GGA			1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly			
515	520	525	
TTC TGT GAC CAT GCT TGG GAG TTC AAA AAA GAA TGC TAC ATA AAG CAT			1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His			
530	535	540	
GGA GAC ACT CTA GAA GTA CCA CCT GAA TGC CAA TAA ATGAACAAAG			1678
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln			
545	550	555	
ATACAGAAGC TAAGACTACT ACAGCAGAAG ATAAAAGAGA AGCTGTAGTT CTTCAAAAC			1738
AGTATATTTT GATGTAACCA TTGTTACTT ACATAAAAAT AAATTGTTAT TATCATAACG			1798
TAAAGAAAAA AAAAAAAA AAAA			1822

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1644
- (D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)

(x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAA AAC ATG GAA AAC GAT GAA AAT ATT GTA GTT GGA CCT AAA CCG	48
Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Val Gly Pro Lys Pro	
1 5 10 15	
TTT TAC CCT ATC GAA GAG GGA TCT GCT GGA ACA CAA TTA CGC AAA TAC	96
Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg Lys Tyr	
20 25 30	
ATG GAG CGA TAT GCA AAA CTT GGC GCA ATT GCT TTT ACA AAT GCA GTT	144
Met Glu Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Val	
35 40 45	
ACT GGT GTT GAT TAT TCT TAC GCC GAA TAC TTG GAG AAA TCA TGT TGT	192
Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys	
50 55 60	
CTA GGA AAA GCT TTG CAA AAT TAT GGT TTG GTT GAT GGC AGA ATT	240
Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val Val Asp Gly Arg Ile	
65 70 75 80	
GCG TTA TGC AGT GAA AAC TGT GAA GAA TTT TTT ATT CCT GTA ATA GCC	288
Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Ile Ala	
85 90 95	
GGA CTG TTT ATA GGT GTA GGT GTT GCA CCC ACT AAT GAG ATT TAC ACT	336
Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr	
100 105 110	
TTA CGT GAA CTG GTT CAC AGT TTA GGT ATC TCT AAA CCA ACA ATT GTA	384
Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val	
115 120 125	
TTT AGT TCT AAA AAA GGC TTA GAT AAA GTT ATA ACA GTA CAG AAA ACA	432
Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr	
130 135 140	
GTA ACT ACT ATT AAA ACC ATT GTT ATA CTA GAT AGC AAA GTT GAT TAT	480
Val Thr Thr Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr	
145 150 155 160	
CGA GGA TAT CAA TGT CTG GAC ACC TTT ATA AAA AGA AAC ACT CCA CCA	528
Arg Gly Tyr Gln Cys Leu Asp Thr Phe Ile Lys Arg Asn Thr Pro Pro	
165 170 175	
GGT TTT CAA GCA TCC AGT TTC AAA ACT GTG GAA GTT GAC CGT AAA GAA	576

Gly	Phe	Gln	Ala	Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	
180								185						190		
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA	624
Gln	Val	Ala	Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	
195							200					205				
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT	672
Gly	Val	Gln	Leu	Thr	His	Glu	Asn	Thr	Val	Thr	Arg	Phe	Ser	His	Ala	
210						215				220						
AGA	GAT	CCG	ATT	TAT	GGT	AAC	CAA	GTT	TCA	CCA	GGC	ACC	GCT	GTT	TTA	720
Arg	Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu	
225						230			235			240				
ACT	GTC	GTT	CCA	TTC	CAT	CAT	GGT	TTT	GGT	ATG	TTC	ACT	ACT	CTA	GGG	768
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	Gly	
245						245			250			255				
TAT	TTA	ATT	TGT	GGT	TTT	CGT	GTT	GTA	ATG	TTA	ACA	AAA	TTC	GAT	GAA	816
Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe	Asp	Glu	
260						260			265			270				
GAA	ACA	TTT	TTA	AAA	ACT	CTA	CAA	GAT	TAT	AAA	TGT	ACA	AGT	GTT	ATT	864
Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr	Ser	Val	Ile	
275						275			280			285				
CTT	GTA	CCG	ACC	TTG	TTT	GCA	ATT	CTC	AAC	AAA	AGT	GAA	TTA	CTC	AAT	912
Leu	Val	Pro	Thr	Leu	Phe	Ala	Ile	Leu	Asn	Lys	Ser	Glu	Leu	Leu	Asn	
290						295			300							
AAA	TAC	GAT	TTG	TCA	AAT	TTA	GTT	GAG	ATT	GCA	TCT	GGC	GGA	GCA	CCT	960
Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Val	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	
305						310			315			320				
TTA	TCA	AAA	GAA	GTT	GGT	GAA	GCT	GTT	GCT	AGA	CGC	TTT	AAT	CTT	CCC	1008
Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	Arg	Arg	Phe	Asn	Leu	Pro	
325						325			330			335				
GGT	GTT	CGT	CAA	GGT	TAT	GGT	TTA	ACA	GAA	ACA	ACA	TCT	GCC	ATT	ATT	1056
Gly	Val	Arg	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Ile	Ile	
340						340			345			350				
ATT	ACA	CCA	GAA	GGA	GAC	GAT	AAA	CCA	GGA	GCT	TCT	GGA	AAA	GTC	GTG	1104
Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys	Pro	Gly	Ala	Ser	Gly	Lys	Val	Val	
355						355			360			365				
CCG	TTG	TTT	AAA	GCA	AAA	GTT	ATT	GAT	CTT	GAT	ACC	AAA	AAA	TCT	TTA	1152
Pro	Leu	Phe	Lys	Ala	Lys	Val	Ile	Asp	Leu	Asp	Thr	Lys	Lys	Ser	Leu	
370						370			375			380				
GGT	CCT	AAC	AGA	CGT	GGA	GAA	GTT	TGT	GTT	AAA	GGA	CCT	ATG	CTT	ATG	1200
Gly	Pro	Asn	Arg	Arg	Gly	Glu	Val	Cys	Val	Lys	Gly	Pro	Met	Leu	Met	
385						390			395			400				
AAA	GGT	TAT	GTA	AAT	AAT	CCA	GAA	GCA	ACA	AAA	GAA	CTT	ATT	GAC	GAA	1248
Lys	Gly	Tyr	Val	Asn	Asn	Pro	Glu	Ala	Thr	Lys	Glu	Leu	Ile	Asp	Glu	
405						405			410			415				
GAA	GGT	TGG	CTG	CAC	ACC	GGA	GAT	ATT	GGA	TAT	TAT	GAT	GAA	GAA	AAA	1296
Glu	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Tyr	Tyr	Asp	Glu	Glu	Lys	
420						420			425			430				
CAT	TTC	TTT	ATT	GTC	GAT	CGT	TTG	AAG	TCT	TTA	ATC	AAA	TAC	AAA	GGA	1344
His	Phe	Phe	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	

435	440	445	
TAC CAA GTA CCA CCT GCC GAA TTA GAA TCC GTT CTT TTG CAA CAT CCA Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro 450	455	460	1392
TCT ATC TTT GAT GCT GGT GTT GCC GGC GTT CCT GAT CCT GTA GCT GGC Ser Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly 465	470	475	1440
GAG CTT CCA GGA GCC GTT GTT GTA CTG GAA AGC GGA AAA AAT ATG ACC Glu Leu Pro GLy Ala Val Val Val Leu Glu Ser Gly Lys Asn Met Thr 485	490	495	1488
GAA AAA GAA GTA ATG GAT TAT GTT GCA AGT CAA GTT TCA AAT GCA AAA Glu Lys Glu Val Met Asp Tyr Val Als Ser Gln Val Ser Asn Ala Lys 500	505	510	1536
CGT TTA CGT GGT GTT CGT TTT GTG GAT GAA GTA CCT AAA GGT CTT Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu 515	520	525	1584
ACT GGA AAA ATT GAC GGC AGA GCA ATT AGA GAA ATC CTT AAG AAA CCA Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro 530	535	540	1632
GTT GCT AAG ATG Val Ala Lys Met 545			1644

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1664
- (D) OTHER INFORMATION: Vargula (cypripidina) luciferase

(x) PUBLICATION INFORMATION:

JP 3-30678 Osaka (Tsuji)

- (A) AUTHORS: Thompson *et al.*
- (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
- (D) VOLUME: 86
- (F) PAGES: 1326-1332
- (G) DATE: (1989)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG AAG ATA ATA ATT CTG TCT GTT ATA TTG GCC TAC TGT GTC ACC GAC Met Lys Ile Ile Ile Leu Ser Val Ile Leu Ala Tyr Cys Val Thr Asp 1 5 10 15	48
AAC TGT CAA GAT GCA TGT CCT GTA GAA GCG GAA CCG CCA TCA AGT ACA Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Pro Pro Ser Ser Thr 20 25 30	96
CCA ACA GTT CCA ACT TCT TGT GAA GCT AAA GAA GGA GAA TGT ATA GAT Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp	144

35	40	45	
ACC AGA TGC GCA ACA TGT AAA CGA GAT ATA CTA TCA GAT GGA CTG TGT Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys 50 55 60			192
GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTG ATT Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile 65 70 75 80			240
GAA TGC AGA GTA GAA GCA GCT GGT TAT TTT AGA ACG TTT TAC GGC AAA Glu Cys Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Gly Lys 85 90 95			288
AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT AGG GGA ACC Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr 100 105 110			336
AAG GGT GGC GAT TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly 115 120 125			384
CAG AAG GGA GCT GTG CTG ACT AAG ACA ACA CTG GAG GTT GCA GGA GAC Gln Lys Gly Ala Val Leu Thr Lys Thr Leu Glu Val Ala Gly Asp 130 135 140			432
GTA ATA GAC ATT ACT CAA GCT ACT GCA GAT CCT ATC ACA GTT AAC GGA Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly 145 150 155 160			480
GGA GCT GAC CCA GTT ATC GCT AAC CCG TTC ACA ATT GGT GAG GTG ACC Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr 165 170 175			528
ATT GCT GTT GTT GAA ATA CCG GGC TTC AAT ATC ACA GTC ATC GAA TTC Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe 180 185 190			576
TTT AAA CTA ATC GTG ATT GAT ATT CTG GGA GGA AGA TCT GTC AGA ATT Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile 195 200 205			624
GCT CCA GAC ACA GCA AAC AAA GGA CTG ATA TCT GGT ATC TGT GGT AAT Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn 210 215 220			672
CTG GAG ATG AAT GAC GCT GAT GAC TTT ACT ACA GAT GCA GAT CAG CTG Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu 225 230 235 240			720
GCG ATC CAA CCC AAC ATA AAC AAA GAG TTC GAC GGC TGC CCA TTC TAT Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr 245 250 255			768
GCG AAT CCT TCT GAT ATC GAA TAC TGC AAA GGT CTG ATG GAG CCA TAC Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr 260 265 270			816
AGA GCT GTA TGT CGT AAC AAT ATC AAC TTC TAC TAT TAC ACT CTA TCC Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser 275 280 285			864
TGT GCC TTC GCT TAC TGT ATG GGA GGA GAA GAA AGA GCT AAA CAC GTC Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val 290 295 300			912

CTT	TTC	GAC	TAT	GTT	GAG	ACA	TGC	GCT	GCG	CCG	GAA	ACG	AGA	GGA	ACG	960
Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
305					310					315					320	
TGT	GTT	TTA	TCA	GGA	CAT	ACT	TTC	TAT	GAC	ACA	TTC	GAC	AAA	GCA	AGA	1008
Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
					325				330					335		
TAT	CAA	TTC	CAG	GGC	CCA	TGC	AAG	GAG	ATT	CTG	ATG	GCC	GCA	GAC	TGT	1056
Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Ile	Leu	Met	Ala	Ala	Asp	Cys	
					340				345					350		
TAC	TGG	AAC	ACA	TGG	GAT	GTA	AAG	GTT	TCA	CAT	AGA	GAC	GTC	GAA	TCA	1104
Tyr	Trp	Asn	Thr	Trp	Asp	Val	Lys	Val	Ser	His	Arg	Asp	Val	Glu	Ser	
					355			360					365			
TAC	ACT	GAG	GTA	GAG	AAA	GTA	ACA	ATC	AGG	AAA	CAG	TCA	ACT	GTA	GTA	1152
Tyr	Thr	Glu	Val	Glu	Lys	Val	Thr	Ile	Arg	Lys	Gln	Ser	Thr	Val	Val	
					370			375					380			
GAT	CTC	ATT	GTG	GAT	GGC	AAG	CAG	GTC	AAG	GTT	GGA	GGA	GTG	GAT	GTA	1200
Asp	Leu	Ile	Val	Asp	Gly	Lys	Gln	Val	Lys	Val	Gly	Gly	Val	Asp	Val	
					385			390					395		400	
TCT	ATC	CCG	TAC	AGC	TCT	GAG	AAC	ACT	TCC	ATA	TAC	TGG	CAG	GAT	GGA	1248
Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly	
					405				410					415		
GAC	ATC	CTG	ACG	ACG	GCC	ATC	CTA	CCT	GAA	GCT	CTT	GTC	GTT	AAG	TTC	1296
Asp	Ile	Leu	Thr	Ala	Ile	Leu	Pro	Glu	Ala	Leu	Val	Val	Val	Lys	Phe	
					420			425					430			
AAC	TTT	AAG	CAG	CTC	CTT	GTA	GTT	CAT	ATC	AGA	GAT	CCA	TTC	GAT	GCA	1344
Asn	Phe	Lys	Gln	Leu	Leu	Val	Val	His	Ile	Arg	Asp	Pro	Phe	Asp	Ala	
					435			440					445			
AAG	ACA	TGC	GGC	ATA	TGT	GGT	AAC	TAT	AAT	CAA	GAT	TCA	ACT	GAT	GAT	1392
Lys	Thr	Cys	Gly	Ile	Cys	Gly	Asn	Tyr	Asn	Gln	Asp	Ser	Thr	Asp	Asp	
					450			455					460			
TTC	TTT	GAC	GCA	GAA	GGA	GCA	TGC	GCT	CTA	ACC	CCC	AAC	CCC	CCA	GGA	1440
Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	
					465			470					475		480	
TGT	ACA	GAG	GAA	CAG	AAA	CCA	GAA	GCT	GAG	CGA	CTT	TGC	AAT	AAT	CTC	1488
Cys	Thr	Glu	Glu	Gln	Lys	Pro	Glu	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Leu	
					485			490					495			
TTT	GAT	TCT	TCT	ATC	GAC	GAG	AAA	TGT	AAT	GTC	TGC	TAC	AAG	CCT	GAC	1536
Phe	Asp	Ser	Ser	Ile	Asp	Glu	Lys	Cys	Asn	Val	Cys	Tyr	Lys	Pro	Asp	
					500			505					510			
CGG	ATT	GCC	CGA	TGT	ATG	TAC	GAG	TAT	TGC	CTG	AGG	GGA	CAA	CAA	GGA	1584
Arg	Ile	Ala	Arg	Cys	Met	Tyr	Glu	Tyr	Cys	Leu	Arg	Gly	Gln	Gln	Gly	
					515			520					525			
TTT	TGT	GAC	CAT	GCT	TGG	GAG	TTC	AAG	AAA	GAA	TGC	TAC	ATA	AAA	CAT	1632
Phe	Cys	Asp	His	Ala	Trp	Glu	Phe	Lys	Lys	Glu	Cys	Tyr	Ile	Lys	His	
					530			535					540			
GGA	GAC	ACT	CTA	GAA	GTA	CCA	CCT	GAA	TGT	CAA	TAA	ACGTACAAAG				1678
Gly	Asp	Thr	Leu	Glu	Val	Pro	Pro	Glu	Cys	Gln						
					545			550					555			
ATACAGAAC	TAAGGCTACT	ACAGCAGAAC	ATAAAAAAAGA	AACTGTAGTT	CCTTCAAAAAA											1738
CCGTGTATTT	TATGTA	CTCA	TTGTTAATT	AGAGCAAAAT	AAATTGTTAT	TATCATAACT										1798

TAAACTAAAAA AAAAAAAA A

1820

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 115...702
- (D) OTHER INFORMATION: apoaequorin-encoding gene

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,093,240
(A) AUTHORS: Inouye *et al.*
(C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
(D) VOLUME: 82
(F) PAGES: 3154-3158
(G) DATE: (1985)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGAAATGCAA TTCATCTTGT CATCAAAGAA 60

TTACATCAAA TCTCTAGTTG ATCAACTAAA TTGTCTCGAC AACACAAGC AAAC ATG 117
Met
1

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AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC AAC 213
Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val Asn
20          25          30

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CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT GAT 261
 His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser Asp
 35 40 45

ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA CAC 309
 Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg His
 50 55 60 65

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AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT      357
Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly
70          75          80

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GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG GCT 405
 Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala
 85 89 95

ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC CGT 453
 Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg
 100 105 110

ATA TGG GGT GAT GCT TTG TTT GAT ATC GTT GAC AAA GAT CAA AAT GGA Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn Gly 115 120 125	501
GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT ATC Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile 130 135 140 145	549
ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp Ile 150 155 160	597
GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His Leu 165 170 175	645
GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly 180 185 190	693
GCT GTC CCC TAAGAAGCTC TACGGTGGTG ATGCACCTA GGAAGATGAT GTGATTTGA 752 Ala Val Pro 195	
ATAAAAACACT GATGAATTCA ATCAAAATTT TCCAAATTT TGAAACGATTT CAATCGTTG TGTTGATTT TGTAATTAGG AACAGATTA ATCGAATGAT TAGTTGTTT TTTAATCAAC AGAACTTACA AATCGAAAAA GTAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAA AAAAAAAA AAAAAA	812 872 932 958

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant Aequorin AEQ1

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.

(B) TITLE: Sequence Comparisons of Complementary
DNAs Encoding Aequorin Isotypes

(C) JOURNAL: Biochemistry

(D) VOLUME: 26

(F) PAGES: 1326-1332

(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn 1 5 10 15	48
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96

Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val			
20	25	30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC			144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser			
35	40	45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT			192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg			
50	55	60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT			240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr			
65	70	75	80
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG			288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu			
85	90	95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT			336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile			
100	105	110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT GAC AAA GAC CAA AAT			384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Asp Lys Asp Gln Asn			
115	120	125	
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GAT GGC			432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Asp Gly			
130	135	140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT			480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp			
145	150	155	160
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT			528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His			
165	170	175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT			576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly			
180	185	190	
GGA GCT GTC CCC TAA			591
Gly Ala Val Pro *			
195			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant Aequorin AEQ2

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.
 (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
 (C) JOURNAL: Biochemistry
 (D) VOLUME: 26
 (F) PAGES: 1326-1332
 (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA TCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Ser Asp Phe Asp Asn	
1 5 10 15	
CCA AGA TGG ATT GGA CGA CAC AAG CAT ATG TTC AAT TTC CTT GAT GTC	96
Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AAA ATC TCT CTT GAC GAG ATG GTC TAC AAG GCA TCT	144
Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTC ATC AAT AAC CTT GGA GCA ACA CCT GAG CAA GCC AAA CGA	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GGA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr	
65 70 75 80	
GGT GTG GAA ACT GAT TGG CCT GCA TAT ATT GAA GGA TGG AAA AAA TTG	288
Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu	
85 90 95	
GCT ACT GAT GAA TTG GAG AAA TAC GCC AAA AAC GAA CCA ACG CTC ATC	336
Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile	
100 105 110	
CGT ATA TGG GGT GAT GCT TTG TTC GAT ATC GTT GAC AAA GAT CAA AAT	384
Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn	
115 120 125	
GGA GCC ATT ACA CTG GAT GAA TGG AAA GCA TAC ACC AAA GCT GCT GGT	432
Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly	
130 135 140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC TAA	591
Gly Ala Val Pro *	
195	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Prasher et al.

(B) TITLE: Sequence Comparisons of Complementary
DNAs Encoding Aequorin Isotypes

(C) JOURNAL: Biochemistry

(D) VOLUME: 26

(F) PAGES: 1326-1332

(G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	TCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	
1									10						15	
CCA	AGA	TGG	ATT	GGA	CGA	CAC	AAG	CAT	ATG	TTC	AAT	TTC	CTT	GAT	GTC	96
Pro	Arg	Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	
20									25						30	
AAC	CAC	AAT	GGA	AAA	ATC	TCT	CTT	GAC	GAG	ATG	GTC	TAC	AAG	GCA	TCT	144
Asn	His	Asn	Gly	Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	
35								40				45				
GAT	ATT	GTC	ATC	AAT	AAC	CTT	GGA	GCA	ACA	CCT	GAG	CAA	GCC	AAA	CGA	192
Asp	Ile	Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	
50							55			60						
CAC	AAA	GAT	GCT	GTA	GGA	GAC	TTC	TTC	GGA	GGA	GCT	GGA	ATG	AAA	TAT	240
His	Lys	Asp	Ala	Val	Gly	Asp	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	
65							70		75				80			
GGT	GTG	GAA	ACT	GAT	TGG	CCT	GCA	TAC	ATT	GAA	GGA	TGG	AAA	AAA	TTG	288
Gly	Val	Glu	Thr	Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	
85							90			95						
GCT	ACT	GAT	GAA	TTG	GAG	AAA	TAC	GCC	AAA	AAC	GAA	CCA	ACG	CTC	ATC	336
Ala	Thr	Asp	Glu	Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	
100							105			110						
CGT	ATA	TGG	GGT	GAT	GCT	TTG	TTC	GAT	ATC	GTT	GAC	AAA	GAT	CAA	AAT	384
Arg	Ile	Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	
115							120			125						
GGA	GCC	ATT	ACA	CTG	GAT	GAA	TGG	AAA	GCA	TAC	ACC	AAA	GCT	GCT	GGT	432
Gly	Ala	Ile	Thr	Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	

130	135	140	
ATC ATC CAA TCA TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT			480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp			
145	150	155	160
ATT GAT GAA AAT GGA CAA CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT			528
Ile Asp Glu Asn Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His			
165	170	175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT			576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly			
180	185	190	190
GGA GCT GTC CCC TAA			591
Gly Ala Val Pro *			
195			

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...567

(D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Charbonneau et al.

(B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin

(C) JOURNAL: Am. Chem. Soc.

(D) VOLUME: 24

(E) ISSUE: 24

(F) PAGES: 6762-6771

(G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC		48	
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His			
1	5	10	15
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT		96	
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser			
20	25	30	
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT		144	
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu			
35	40	45	
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC		192	
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala			

50	55	60														
TTC	TTC	GGA	GGA	GCT	GCA	ATG	AAA	TAT	GGT	GTA	GAA	ACT	GAA	TGG	CCT	240
Phe	Phe	Gly	Gly	Ala	Ala	Met	Lys	Tyr	Gly	Val	Glu	Thr	Glu	Trp	Pro	
65						70				75					80	
GAA	TAC	ATC	GAA	GGA	TGG	AAA	AGA	CTG	GCT	TCC	GAG	GAA	TTG	AAA	AGG	288
Glu	Tyr	Ile	Glu	Gly	Trp	Lys	Arg	Leu	Ala	Ser	Glu	Glu	Leu	Lys	Arg	
						85				90				95		
TAT	TCA	AAA	AAC	CAA	ATC	ACA	CTT	ATT	CGT	TTA	TGG	GGT	GAT	GCA	TTG	336
Tyr	Ser	Lys	Asn	Gln	Ile	Thr	Leu	Ile	Arg	Leu	Trp	Gly	Asp	Ala	Leu	
						100				105				110		
TTC	GAT	ATC	ATT	GAC	AAA	GAC	CAA	AAT	GGA	GCT	ATT	TCA	CTG	GAT	GAA	384
Phe	Asp	Ile	Ile	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Ser	Leu	Asp	Glu	
						115			120				125			
TGG	AAA	GCA	TAC	ACC	AAA	TCT	GCT	GGC	ATC	ATC	CAA	TCG	TCA	GAA	GAT	432
Trp	Lys	Ala	Tyr	Thr	Lys	Ser	Ala	Gly	Ile	Ile	Gln	Ser	Ser	Glu	Asp	
						130			135			140				
TGC	GAG	GAA	ACA	TTC	AGA	GTG	TGC	GAT	ATT	GAT	GAA	AGT	GGA	CAG	CTC	480
Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser	Gly	Gln	Leu	
						145			150			155		160		
GAT	GTT	GAT	GAG	ATG	ACA	AGA	CAA	CAT	TTA	GGA	TTT	TGG	TAC	ACC	ATG	528
Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp	Tyr	Thr	Met	
						165			170			175				
GAT	CCT	GCT	TGC	GAA	AAG	CTC	TAC	GGT	GGA	GCT	GTC	CCC				567
Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly	Ala	Val	Pro				
						180			185							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Aequorin mutant w/increased

bioluminescence activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 10:

Asp 124 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	

1	5	10	15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC				96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val				
20	25	30		
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC				144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser				
35	40	45		
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT				192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg				
50	55	60		
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT				240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr				
65	70	75	80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG				288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu				
85	90	95		
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT				336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile				
100	105	110		
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT				384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn				
115	120	125		
GGA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC				432
Gly Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly				
130	135	140		
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT				480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp				
145	150	155	160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT				528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His				
165	170	175		
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT				576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly				
180	185	190		
GGA GCT GTC CCC				588
Gly Ala Val Pro				
195				

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...588
 (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant
 w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 11:
 Glu 135 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GGA GCT ATT TCA CTG GAT TCA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Gly Ala Ile Ser Leu Asp Ser Trp Lys Ala Tyr Thr Lys Ser Ala Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	
ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...588

(D) OTHER INFORMATION: Recombinant site-directed
Aequorin mutant w/increased biolum. activity

(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC	48
Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn	
1 5 10 15	
CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC	96
Pro Lys Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val	
20 25 30	
AAC CAC AAT GGA AGG ATC TCT CTT GAC GAG ATG GTC TAC AAG GCG TCC	144
Asn His Asn Gly Arg Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser	
35 40 45	
GAT ATT GTT ATA AAC AAT CTT GGA GCA ACA CCT GAA CAA GCC AAA CGT	192
Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg	
50 55 60	
CAC AAA GAT GCT GTA GAA GCC TTC TTC GGA GGA GCT GCA ATG AAA TAT	240
His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Ala Met Lys Tyr	
65 70 75 80	
GGT GTA GAA ACT GAA TGG CCT GAA TAC ATC GAA GGA TGG AAA AGA CTG	288
Gly Val Glu Thr Glu Trp Pro Glu Tyr Ile Glu Gly Trp Lys Arg Leu	
85 90 95	
GCT TCC GAG GAA TTG AAA AGG TAT TCA AAA AAC CAA ATC ACA CTT ATT	336
Ala Ser Glu Glu Leu Lys Arg Tyr Ser Lys Asn Gln Ile Thr Leu Ile	
100 105 110	
CGT TTA TGG GGT GAT GCA TTG TTC GAT ATC ATT TCC AAA GAC CAA AAT	384
Arg Leu Trp Gly Asp Ala Leu Phe Asp Ile Ile Ser Lys Asp Gln Asn	
115 120 125	
GCA GCT ATT TCA CTG GAT GAA TGG AAA GCA TAC ACC AAA TCT GCT GGC	432
Ala Ala Ile Ser Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ser Ala Gly	
130 135 140	
ATC ATC CAA TCG TCA GAA GAT TGC GAG GAA ACA TTC AGA GTG TGC GAT	480
Ile Ile Gln Ser Ser Glu Asp Cys Glu Thr Phe Arg Val Cys Asp	
145 150 155 160	

ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT	528
Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His	
165 170 175	
TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT	576
Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly	
180 185 190	
GGA GCT GTC CCC	588
Gly Ala Val Pro	
195	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...567
- (D) OTHER INFORMATION: Recombinant apoaequorin (AQUALITE[®])

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTC AAG CTT ACA CCA GAC TTC GAC AAC CCA AAA TGG ATT GGA CGA CAC	48
Val Lys Leu Thr Pro Asp Phe Asp Asn Pro Lys Trp Ile Gly Arg His	
1 5 10 15	
AAG CAC ATG TTT AAT TTT CTT GAT GTC AAC CAC AAT GGA AGG ATC TCT	96
Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Arg Ile Ser	
20 25 30	
CTT GAC GAG ATG GTC TAC AAG GCG TCC GAT ATT GTT ATA AAC AAT CTT	144
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu	
35 40 45	
GGA GCA ACA CCT GAA CAA GCC AAA CGT CAC AAA GAT GCT GTA GAA GCC	192
Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala	
50 55 60	
TTC TTC GGA GGA GCT GGA ATG AAA TAT GGT GTA GAA ACT GAA TGG CCT	240
Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Glu Trp Pro	
65 70 75 80	
GAA TAC ATC GAA GGA TGG AAA AAA CTG GCT TCC GAG GAA TTG AAA AGG	288
Glu Tyr Ile Glu Gly Trp Lys Lys Leu Ala Ser Glu Glu Leu Lys Arg	
85 90 95	
TAT TCA AAA AAC CAA ATC ACA CTT ATT CGT TTA TGG GGT GAT GCA TTG	336
Tyr Ser Lys Asn Gln Ile Thr Leu Ile Arg Leu Trp Gly Asp Ala Leu	
100 105 110	
TTC GAT ATC ATT GAC AAA GAC CAA AAT GGA GCT ATT CTG TCA GAT GAA	384
Phe Asp Ile Ile Asp Lys Asp Gln Asn Gly Ala Ile Leu Ser Asp Glu	
115 120 125	
TGG AAA GCA TAC ACC AAA TCT GAT GGC ATC ATC CAA TCG TCA GAA GAT	432
Trp Lys Ala Tyr Thr Lys Ser Asp Gly Ile Ile Gln Ser Ser Glu Asp	
130 135 140	

TGC GAG GAA ACA TTC AGA GTG TGC GAT ATT GAT GAA AGT GGA CAG CTC	480
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu	
145 150 155 160	
GAT GTT GAT GAG ATG ACA AGA CAA CAT TTA GGA TTT TGG TAC ACC ATG	528
Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met	
165 170 175	
GAT CCT GCT TGC GAA AAG CTC TAC GGT GGA GCT GTC CCC	567
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro	
180 185	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x) PUBLICATION INFORMATION:
PATENT NO.: 5,484,723

(ix) FEATURE:
(D) OTHER INFORMATION: *Vibrio fisheri* Flavin reductase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn
1 5 10 15

Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala
20 25 30

Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
35 40 45

Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His
50 55 60

Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser
65 70 75 80

Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro
85 90 95

His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu
100 105 110

Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
115 120 125

Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly
130 135 140

Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala
145 150 155 160

Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu
165 170 175

Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp

180

185

190

Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
195 200 205

Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys
210 215 220

Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile
225 230 235